Amendments to the Specification:

Please amend the specification as shown:

Page 1, before the heading entitled "TECHNICAL FIELD", insert the following new paragraph:

This invention was made with Government support under Grant Nos. AG17556 and AG00745 awarded by the National Institutes of Health. The Government has certain rights in the invention.

Please delete the paragraph on page 3, line 24 to page 4, line 10 and replace it with the following paragraph:

Figure 2. Seven-transmembrane-spanning model of human α_{1a}AR showing the primary amino acid sequence **(SEQ ID NO: 1)**. Key residues are colored including SNP sites (yellow, with amino acid number listed next to SNP), and important residues for agonist binding (red) and antagonist binding (green). The salt bridge is formed between D106 (red and blue, also identified as an important residue in agonist binding) in TM3 and K309 (blue) in TM7. This model was based on the results of several mutagenesis studies (Hwa et al, J. Biol. Chem. 270:23189-23195 (1995), Hwa et al, J. Biol. Chem. 271:6322-6327 (1996), Porter et al, J. Biol. Chem. 271:28318-28323 (1996), Waugh et al, J. Biol. Chem. 275:11698-11705 (2000), Waugh et al, J. Biol. Chem. 276:α125366-25371 (2001), Zhao et al, Mol. Pharmacol. 50:118-1126 (1996), Chen et al, J. Biol. Chem. 274:16320-16330 (1999), Hamaguchi et al, Biochemistry 35:14312-14317 (1996)).

Please delete the paragraph on page 6, line 25 to page 7, line 16 and replace it with the following paragraph:

DNA was sequenced from individuals at the highest and lowest blood pressures (5000bp DNA from n=281 total individuals was sequenced using rapid throughput DNA sequencers). As a result, 49 genetic variants of the human α_{1a}AR have been identified over the 5kb of sequence investigated, 46 of which are single nucleotide polymorphisms (SNPs), 1 insertion/deletion, and 3 microsatellite repeats. The exact location of these genetic variants is shown in Table 1 **(nucleotide sequences of 10 or more bp are shown in SEQ ID NOS 2-37, respectively, in order of appearance)**(the α_{1a}AR gene has 2 major exons and 3 additional splice variants in addition to the originally described wild type sequence (Table 2 – **(SEQ ID NO: 38)** 1st exon with its 5'-regulatory/UTR and 3' intron sequence, Table 3 **(SEQ ID NOS 39-40)** - 2nd exon with associated 5' intron and 3' sequences (splice variant a-1 is part of exon 2 sequence), Table 4 **(SEQ ID NOS 41-42)** - splice variant a-4 and its associated 5' and 3' nucleotides, Table 5 **(SEQ ID NOS 43-44)** - splice variant a-3 with its associated 5'/3' sequences (see also schematic is shown in Figure 1). As detailed in the Example below, cDNAs expressing the coding region SNPs that alter amino acid sequence have been prepared and characterized for biologic function; biologic effects in terms of ligand binding to agonists or antagonists are described, as is the association of one coding region SNP with altered cell growth. (Two SNPs have been reported in dbSNP - A6804 (I200S, released on 8/15/01) and A6944 (G247R, released on 8/28/02) - there is no reference to any function, confirmation, or association with disease for either of these SNPs.)

Before the Figures, insert the Sequence Listing submitted herewith on separate sheets.